```
                          1                                                    50
HGRA4sv.cds     (1)   ATGACAACTCTTGTTCCTGCAACCCTCTCCTTCCTTCTTCTCTGGACCCT
SEQ ID NO:23    (1)   --------------------------------------------------

                      51                                                   100
HGRA4sv.cds    (51)   GCCAGGGCAGGTCCTCCTCAGGGTGGCCTTGGCAAAAGAGGAAGTCAAAT
SEQ ID NO:23    (1)   ------------------AGGGTGGCCTTGGCAAAAGAGGAAGTCAAAT

                      101                                                  150
HGRA4sv.cds   (101)   CTGGAACCAAGGGGTCCCAGCCCATGTCCCCCTCTGATTTCCTAGACAAA
SEQ ID NO:23   (32)   CTGGAACCAAGGGGTCCCAGCCCATGTCCCCCTCTGATTTCCTAGACAAA

                      151                                                  200
HGRA4sv.cds   (151)   CTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCAATTTTAA
SEQ ID NO:23   (82)   CTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCAATTTTAA

                      201                                                  250
HGRA4sv.cds   (201)   AGGCCCACCCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCT
SEQ ID NO:23  (132)   AGGCCCACCCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCT

                      251                                                  300
HGRA4sv.cds   (251)   CCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAA
SEQ ID NO:23  (182)   CCATCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAA

                      301                                                  350
HGRA4sv.cds   (301)   CAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCT
SEQ ID NO:23  (232)   CAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCT

                      351                                                  400
HGRA4sv.cds   (351)   GGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCT
SEQ ID NO:23  (282)   GGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCT

                      401                                                  450
HGRA4sv.cds   (401)   TTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAG
SEQ ID NO:23  (332)   TTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAG

                      451                                                  500
HGRA4sv.cds   (451)   TTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGAC
SEQ ID NO:23  (382)   TTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGAC

                      501                                                  550
HGRA4sv.cds   (501)   CCTCATTTTGTCCTGCCTGATGGACCTCAAGAACTTCCCCATGGACATCC
SEQ ID NO:23  (432)   CCTCATTTTGTCCTGCCTGATGGACCTCAAGAACTTCCCCATGGACATCC

                      551                                                  600
HGRA4sv.cds   (551)   AGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTG
SEQ ID NO:23  (482)   AGACCTGCACGATGCAGCTTGAGAGCT-----------------------

                      601                                                  650
HGRA4sv.cds   (601)   CCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTTGA
SEQ ID NO:23  (509)   ------------------TTGGCTACACCATGAAAGACCTCGTGTTTGA

                      651                                                  700
HGRA4sv.cds   (651)   GTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGC
SEQ ID NO:23  (540)   GTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGC

                      701                                                  750
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HGRA4sv.cds  (701) CCCAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCAC
SEQ ID NO:23 (590) CCCAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCAC

                   751                                              800
HGRA4sv.cds  (751) TACAACACAGGGAAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACG
SEQ ID NO:23 (640) TACAACACAGGGAAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACG

                   801                                              850
HGRA4sv.cds  (801) GCAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCG
SEQ ID NO:23 (690) GCAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCG

                   851                                              900
HGRA4sv.cds  (851) TCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCCTGCC
SEQ ID NO:23 (740) TCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCCTGCC

                   901                       .                      950
HGRA4sv.cds  (901) CGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCCAGAGCTC
SEQ ID NO:23 (790) CGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCCAGAGCTC

                   951                                             1000
HGRA4sv.cds  (951) TGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACA
SEQ ID NO:23 (840) TGGCTCCCGGGCCTCTTTGCCTAAGGTG----------------------

                   1001                                            1050
HGRA4sv.cds (1001) TCTGGATGGCTGTGTGTCTGCTCTTTGTGTTCGCTGCCTTGCTGGAGTAT
SEQ ID NO:23 (868) --------------------------------------------------

                   1051                                            1100
HGRA4sv.cds (1051) GCTGCCATAAATTTTGTTTCTCGTCAGCATAAAGAATTCATACGACTTCG
SEQ ID NO:23 (868) --------------------------------------------------

                   1101                                            1150
HGRA4sv.cds (1101) AAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATCCAAGAAAGTC
SEQ ID NO:23 (868) --------------------------------------------------

                   1151                                            1200
HGRA4sv.cds (1151) GTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGGCAAGAGAT
SEQ ID NO:23 (868) --------------------------------------------------

                   1201                                            1250
HGRA4sv.cds (1201) GGAGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTCCAGCCCC
SEQ ID NO:23 (868) --------------------------------------------------

                   1251                                  1293
HGRA4sv.cds (1251) TCTTCTAAGGGAAGGAGAAACCACGCGGAAACTCTACGTGGAC
SEQ ID NO:23 (868) -------------------------------------------
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                            1                                              50
HGRA4sv.cds       (1) ATGACAACTCTTGTTCCTGCAACCCTCTCCTTCCTTCTTCTCTGGACCCT
SEQ ID NO:55      (1) --------------------------------------------------

                            51                                            100
HGRA4sv.cds      (51) GCCAGGGCAGGTCCTCCTCAGGGTGGCCTTGGCAAAAGAGGAAGTCAAAT
SEQ ID NO:55      (1) --------------------------------------------------

                            101                                           150
HGRA4sv.cds     (101) CTGGAACCAAGGGGTCCCAGCCCATGTCCCCCTCTGATTTCCTAGACAAA
SEQ ID NO:55      (1) --------------------------------------------------

                            151                                           200
HGRA4sv.cds     (151) CTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCAATTTTAA
SEQ ID NO:55      (1) --------------------------------------------------

                            201                                           250
HGRA4sv.cds     (201) AGGCCCACCCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCT
SEQ ID NO:55      (1) --------------------------------------------------

                            251                                           300
HGRA4sv.cds     (251) CCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAA
SEQ ID NO:55      (1) --------------------------------------------------

                            301                                           350
HGRA4sv.cds     (301) CAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCT
SEQ ID NO:55      (1) --------------------------------------------------

                            351                                           400
HGRA4sv.cds     (351) GGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCT
SEQ ID NO:55      (1) --------------------------------------------------

                            401                                           450
HGRA4sv.cds     (401) TTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAG
SEQ ID NO:55      (1) --------------------------------------------------

                            451                                           500
HGRA4sv.cds     (451) TTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGAC
SEQ ID NO:55      (1) --------------------------------------------------

                            501                                           550
HGRA4sv.cds     (501) CCTCATTTTGTCCTGCCTGATGGACCTCAAGAACTTCCCCATGGACATCC
SEQ ID NO:55      (1) --------------------------------------------------

                            551                                           600
HGRA4sv.cds     (551) AGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTG
SEQ ID NO:55      (1) --------------------------------------------------

                            601                                           650
HGRA4sv.cds     (601) CCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTTGA
SEQ ID NO:55      (1) --------------------------------------------------

                            651                                           700
HGRA4sv.cds     (651) GTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGC
SEQ ID NO:55      (1) --------------------------------------------------

                            701                                           750
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HGRA4sv.cds   (701)  CCCAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCAC
SEQ ID NO:55    (1)  --------------------------------------------------

                     751                                              800
HGRA4sv.cds   (751)  TACAACACAGGGAAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACG
SEQ ID NO:55    (1)  --------------------------------------------------

                     801                                              850
HGRA4sv.cds   (801)  GCAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCG
SEQ ID NO:55    (1)  --------------------------------------------------

                     851                                              900
HGRA4sv.cds   (851)  TCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCCTGCC
SEQ ID NO:55    (1)  --------------------------------------------------

                     901                                              950
HGRA4sv.cds   (901)  CGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCCAGAGCTC
SEQ ID NO:55    (1)  --------------------------------------------------

                     951                                             1000
HGRA4sv.cds   (951)  TGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACA
SEQ ID NO:55    (1)  --------------------------------------------------

                     1001                                            1050
HGRA4sv.cds  (1001)  TCT GGATGGCTGTGTGTCTGCTCTTTGTGTTCGCTGCCTTGCTGGAGTAT
SEQ ID NO:55    (1)  --- GGATGGCTGTGTGTCTGCTCTTTGTGTTCGCTGCCTTGCTGGAGTAT

                     1051                                            1100
HGRA4sv.cds  (1051)  GCTGCCATAAATTTTGTTTCTCGTCAGCATAAAGAATTCATACGACTTCG
SEQ ID NO:55   (48)  GCTGCCATAAATTTTGTTTCTCGTCAGCATAAAGAATTCATACGACTTCG

                     1101                                            1150
HGRA4sv.cds  (1101)  AAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATCCAAGAAAGTC
SEQ ID NO:55   (98)  AAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATCCAAGAAAGTC

                     1151                                            1200
HGRA4sv.cds  (1151)  GTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGGCAAGAGAT
SEQ ID NO:55  (148)  GTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGGCAAGAGAT

                     1201                                            1250
HGRA4sv.cds  (1201)  GGAGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTCCAGCCCC
SEQ ID NO:55  (198)  GGAGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTCCAGCCCC

                     1251                                            1300
HGRA4sv.cds  (1251)  TCTTCTAAGGGAAGGAGAAACCACGCGGAAACTCTACGTGGAC-------
SEQ ID NO:55  (248)  TCTTCTAAGGGAAGGAGAAACCACGCGGAAACTCTACGTGGAC TGAGCCA

                     1301                                            1350
HGRA4sv.cds  (1294)  --------------------------------------------------
SEQ ID NO:55  (298)  AGAGAATTGACACCATCTCCCGGGCTGTCTTCCCTTTCACTTTCCTCATC

                     1351                                            1400
HGRA4sv.cds  (1294)  --------------------------------------------------
SEQ ID NO:55  (348)  TTCAATATCTTCTACTGGGTTGTCTATAAAGTGCTATGGTCAGAAGNTAN
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                              1401                    .                      1450
    HGRA4sv.cds  (1294) --------------------------------------------------
    SEQ ID NO:55  (398) CCACCAGGCTCTGTGAATAGGGTGGGAGCTATAGAGTCCTGCTGCTGGCC


                              1451                                          1500
    HGRA4sv.cds  (1294) --------------------------------------------------
    SEQ ID NO:55  (448) TCCTGCTTCCTCCTGGGTGGGNTTTCTCCCTCAGTTAGACTCCATTAGGG


                              1501                                          1550
    HGRA4sv.cds  (1294) --------------------------------------------------
    SEQ ID NO:55  (498) GTTTGGACAGTTCCTTCCTGATCTCCCANTCAGAACTTCATCTACCAGTN


                              1551                1575
    HGRA4sv.cds  (1294) -------------------------
    SEQ ID NO:55  (548) CCAAAGCTATGTGGGCCTATATTGC
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                              1                                                50
         HGRA4sv     (1)   MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPMSPSDFLDK
       SEQ ID NO:41  (1)   -------------------------------------------------
       SEQ ID NO:50  (1)   ----------------------RVALAKEEVKSGTKGSQPMSPSDFLDK

                              51                                              100
         HGRA4sv    (51)   LMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQ
       SEQ ID NO:41  (1)   -------------------------------------------------
       SEQ ID NO:50 (28)   LMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSITKTTMDYRVNVFLRQ

                              101                                             150
         HGRA4sv   (101)   QWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNK
       SEQ ID NO:41  (1)   -------------------------------------------------
       SEQ ID NO:50 (78)   QWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNK

                              151                                             200
         HGRA4sv   (151)   LLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPL
       SEQ ID NO:41  (1)   -------------------------------------------------
       SEQ ID NO:50 (128)  LLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLES--------

                              201                                             250
         HGRA4sv   (201)   PSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKH
       SEQ ID NO:41  (1)   -------------------------------------------------
       SEQ ID NO:50 (170)  ------FGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKH

                              251                                             300
         HGRA4sv   (251)   YNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPA
       SEQ ID NO:41  (1)   -------------------------------------------------
       SEQ ID NO:50 (214)  YNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPA

                              301                                             350
         HGRA4sv   (301)   RVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEY
       SEQ ID NO:41  (1)   -------------------------VSYVKAIDIWMAVCLLFVFAALLEY
       SEQ ID NO:50 (264)  RVGLGITTVLTMTTQSSGSRASLPKV------------------------

                              351                                             400
         HGRA4sv   (351)   AAINFVSRQHKEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHCLQARD
       SEQ ID NO:41 (26)   AAINFVSRQHKEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHCLQARD
       SEQ ID NO:50 (290)  -------------------------------------------------

                              401                                             450
         HGRA4sv   (401)   GGPMEGSGIYSPQPPAPLLREGETTRKLYVD------------------
       SEQ ID NO:41 (76)   GGPMEGSGIYSPQPPAPLLREGETTRKLYVDAKRIDTISRAVFPFTFLIF
       SEQ ID NO:50 (290)  -------------------------------------------------

                              451            468
         HGRA4sv   (432)   ------------------
       SEQ ID NO:41 (126)  NIFYWVVYKVLWSEDIHQ
       SEQ ID NO:50 (290)  ------------------
```

```
                         1                                                      50
HGRA4sv.cds       (1)  ATGACAACTCTTGTTCCTGCAACCCTCTCCTTCCTTCTTCTCTGGACCCT
SEQ ID NO:14      (1)  --------------------------------------------------

                         51                                                    100
HGRA4sv.cds      (51)  GCCAGGGCAGGTCCTCCTCAGGGTGGCCTTGGCAAAAGAGGAAGTCAAAT
SEQ ID NO:14      (1)  --------------------------------------------------

                         101                                                   150
HGRA4sv.cds     (101)  CTGGAACCAAGGGGTCCCAGCCCATGTCCCCCTCTGATTTCCTAGACAAA
SEQ ID NO:14      (1)  --------------------------------------------------

                         151                                                   200
HGRA4sv.cds     (151)  CTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCAATTTTAA
SEQ ID NO:14      (1)  --------------------------------------------------

                         201                                                   250
HGRA4sv.cds     (201)  AGGCCCACCCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCT
SEQ ID NO:14      (1)  --------------------------------------------------

                         251                                                   300
HGRA4sv.cds     (251)  CCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAA
SEQ ID NO:14      (1)  --------------------------------------------------

                         301                                                   350
HGRA4sv.cds     (301)  CAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCT
SEQ ID NO:14      (1)  --------------------------------------------------

                         351                                                   400
HGRA4sv.cds     (351)  GGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCT
SEQ ID NO:14      (1)  --------------------------------------------------

                         401                                                   450
HGRA4sv.cds     (401)  TTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAG
SEQ ID NO:14      (1)  --------------------------------------------------

                         451                                                   500
HGRA4sv.cds     (451)  TTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGAC
SEQ ID NO:14      (1)  --------------------------------------------------

                         501                                                   550
HGRA4sv.cds     (501)  CCTCATTTTGTCCTGCCTGATGGACCTCAAGAACTTCCCCATGGACATCC
SEQ ID NO:14      (1)  --------------------------------------------------

                         551                                                   600
HGRA4sv.cds     (551)  AGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTG
SEQ ID NO:14      (1)  --------------------------------------------------

                         601                                                   650
HGRA4sv.cds     (601)  CCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTTGA
SEQ ID NO:14      (1)  --------------------------------------------------

                         651                                                   700
HGRA4sv.cds     (651)  GTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGC
SEQ ID NO:14      (1)  --------------------------------------------------

                         701                                                   750
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HGRA4sv.cds    (701)  CCCAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCAC
SEQ ID NO:14     (1)  --------------------------------------------------

                      751                                            800
HGRA4sv.cds    (751)  TACAACACAGGGAAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACG
SEQ ID NO:14     (1)  --------------------------------------------------

                      801                                            850
HGRA4sv.cds    (801)  GCAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCG
SEQ ID NO:14     (1)  --------------------------------------------------

                      851                                            900
HGRA4sv.cds    (851)  TCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCCTGCC
SEQ ID NO:14     (1)  --------------------------------------------------

                      901                                            950
HGRA4sv.cds    (901)  CGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCCAGAGCTC
SEQ ID NO:14     (1)  --------------------------------------------------

                      951                                           1000
HGRA4sv.cds    (951)  TGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACA
SEQ ID NO:14     (1)  ----------------------GTGTCCTACGTGAAGGCAATCGACA

                      1001                                          1050
HGRA4sv.cds   (1001)  TCTGGATGGCTGTGTGTCTGCTCTTTGTGTTCGCTGCCTTGCTGGAGTAT
SEQ ID NO:14    (26)  TCTGGATGGCTGTGTGTCTGCTCTTTGTGTTCGCTGCCTTGCTGGAGTAT

                      1051                                          1100
HGRA4sv.cds   (1051)  GCTGCCATAAATTTTGTTTCTCGTCAGCATAAAGAATTCATACGACTTCG
SEQ ID NO:14    (76)  GCTGCCATAAATTTTGTTTCTCGTCAGCATAAAGAATTCATACGACTTCG

                      1101                                          1150
HGRA4sv.cds   (1101)  AAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATCCAAGAAAGTC
SEQ ID NO:14   (126)  AAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATCCAAGAAAGTC

                      1151                                          1200
HGRA4sv.cds   (1151)  GTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGGCAAGAGAT
SEQ ID NO:14   (176)  GTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGGCAAGAGAT

                      1201                                          1250
HGRA4sv.cds   (1201)  GGAGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTCCAGCCCC
SEQ ID NO:14   (226)  GGAGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTCCAGCCCC

                      1251                                          1300
HGRA4sv.cds   (1251)  TCTTCTAAGGGAAGGAGAAACCACGCGGAAACTCTACGTGGAC-------
SEQ ID NO:14   (276)  TCTTCTAAGGGAAGGAGAAACCACGCGGAAACTCTACGTGGACTGAGCCA

                      1301                                          1350
HGRA4sv.cds   (1294)  --------------------------------------------------
SEQ ID NO:14   (326)  AGAGAATTGACACCATCTCCCGGGCTGTCTTCCCTTTCACTTTCCTCATC

                      1351                                          1400
HGRA4sv.cds   (1294)  --------------------------------------------------
SEQ ID NO:14   (376)  TTCAATATCTTCTACTGGGTTGTCTATAAAGTGCTATGGTCAGAAGATAT
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                                    1401
    HGRA4sv.cds    (1294) -------
    SEQ ID NO:14    (426) CCACCAG
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